

COMPOSITIONS AND METHODS FOR PARSING GENE STRUCTUREABSTRACT OF THE DISCLOSURE

The invention provides a method for determining a sequence boundary. The method includes the steps of

5 (a) contacting a population of addressed fragments of eukaryotic genomic DNA with a target polynucleotide, the target polynucleotide binding a terminal sequence of a DNA region, the addressed fragments of eukaryotic genomic DNA being at least 100 nucleotides in length; (b)

10 determining a relative order for 2 or more of the addressed fragments compared to a sequence of the genomic DNA; (c) identifying a pair of fragments among the 2 or more addressed fragments that alternatively bind the terminal sequence of a region; and (d) determining for

15 the sequence of the genomic DNA a relative location of a boundary of the region compared to a location of at least one genomic DNA fragment in the pair.

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